UniProtKB/Swiss-Prot entry 084883

Entry information

Entry name
Primary accession number
Secondary accession numbers
Integrated into Swiss-Prot on
April 27, 2001

Sequence was last modified on November 1, 1998 (Sequence version 1)

Annotations were last modified on October 31, 2006 (Entry version 28)

Name and origin of the protein

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia. Chlamydia trachomatis [TaxID: 813] [HAMAP proteome] OrderedLocusNames: CT_875 Protein CT 875 Protein name Gene name Synonyms Taxonomy From

References

[1]NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=D/UW-3/Cx;

DOI=10.1126/science.282.5389.754; PubMed=9784136

Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;

"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";

Science 282:754-759(1998).

Comments

SIMILARITY: To C.muridarum TC 0268.

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Cross-references

Sequence databases	Ses
EMBL	AE001273; AAC68473.1; -; Genomic_DNA.
PIR	C71460; C71460.
2D gel databases	S
PHCI-2DPAGE 084883;	084883;
Genome annotation databases	tion databases
GenomeReview:	SenomeReviews AE001273_GR; CT_875.
KEGG	ctr:CT875;
Other	
Implicit links to	mplicit links to CMR; ProDom; HOGENOM; BLOCKS; ProtoNet; ModBase; UniRef.

Keywords

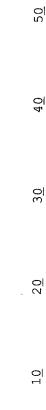
Complete proteome.

Features

FTIG	PRO_0000218349			
Description	Protein CT_875.			
From To Length	591			
or ric	591			
Fr	Н			
Key	CHAIN			

Sequence information

Length: **591 AA** [This is the length of the unprocessed precursor] Molecular weight: **66076 Da** [This is the MW of the unprocessed precursor] CRC64: **B21C0127FDBB2EC8** [This is a checksum on the sequence]



<u>0</u>9

RESPYAVVDV	12 <u>0</u> SSATRAAESG	18 <u>0</u> DVNEARLMAA	24 <u>0</u> LGRRTPNYQS	30 <u>0</u> aratleesmp	36 <u>0</u> FQSFVNECNS	42 <u>0</u> SPEGASLAET	48 <u>0</u> VMDMDLETRR	54 <u>0</u> GFREAVYASF	កា
SLYSSRSNEN	11 <u>0</u>	17 <u>0</u>	23 <u>0</u>	29 <u>0</u>	35 <u>0</u>	41 <u>0</u>	47 <u>0</u>	53 <u>0</u>	59 <u>0</u>
	CAWSSVSTRR	SPMAGVFGNL	GAARKLLNDP	LSREIQTGLR	AQGPSRAQQA	THRYAPRDDL	IYEIMMPIYE	YQLQNMDVEA	MRRWNREVDR
GNNKVEDRVC	10 <u>0</u>	16 <u>0</u>	22 <u>0</u>	28 <u>0</u>	34 <u>0</u>	40 <u>0</u>	46 <u>0</u>	52 <u>0</u>	58 <u>0</u>
	VADKVRRAVQ	FWRTRVLRQT	EQRVRDLQDK	LDMSNLSDVV	ESASRMEGDE	RRCFSCCKGS	PSIEGEGSDS	PYPTPPLPPR	TNGSQTFRDL
GSNRRSQNTK	9 <u>0</u>	15 <u>0</u>	21 <u>0</u>	27 <u>0</u>	33 <u>0</u>	39 <u>0</u>	45 <u>0</u>	51 <u>0</u>	57 <u>0</u>
	FSRFQRGLVR	ARGLRLMFTD	AAAREIAKRW	NLQNVDTGFW	TEIEESGWTR	RGLAAAGEAI	PLVDDWRRGV	RASDYDLPRS	QVEGILRDML
NSRIPSHNGD	8 <u>0</u>	14 <u>0</u>	20 <u>0</u>	26 <u>0</u>	32 <u>0</u>	38 <u>0</u>	44 <u>0</u>	50 <u>0</u>	56 <u>0</u>
	GETTRASRGV	SGYREYSPSA	ANKLAGPDGV	SMFYDGPQVA	RLQETCDAAR	HVRVLCARVS	ERGADGTYDI	DPRASDYDLP	QPQERIPNSQ
MSIRGVGGNG	7 <u>0</u>	13 <u>0</u>	19 <u>0</u>	25 <u>0</u>	31 <u>0</u>	37 <u>0</u>	43 <u>0</u>	49 <u>0</u>	55 <u>0</u>
	SSMIESTPTS	SSSRTARGAS	YTSECADHLE	KNPGEYTVGN	MLENLEERFR	IEFSFGSFGE	Larfaddmgi	SFAVQQGHYQ	VAGMYNYVVT